

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/441,723DATE: 02/21/2001
TIME: 23:50:49

INPUT SET: S36415.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

H7

SEQUENCE LISTING

(1) General Information

ENTERED

(i) APPLICANT: Shah, Purvi
Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.

(ii) TITLE OF THE INVENTION: NEW GLUTATHIONE-S-TRANSFERASE

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/441,723
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/978,174
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0430 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BLADTUT04

(B) CLONE: 1554593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Gly Pro Leu Pro Arg Thr Val Glu Leu Phe Tyr Asp Val Leu Ser
 1           5           10           15
Pro Tyr Ser Trp Leu Gly Phe Glu Ile Leu Cys Arg Tyr Gln Asn Ile
 20           25           30
Trp Asn Ile Asn Leu Gln Leu Arg Pro Ser Leu Ile Thr Gly Ile Met
 35           40           45
Lys Asp Ser Gly Asn Lys Pro Pro Gly Leu Leu Pro Arg Lys Gly Leu
 50           55           60
Tyr Met Ala Asn Asp Leu Lys Leu Leu Arg His His Leu Gln Ile Pro
 65           70           75           80
Ile His Phe Pro Lys Asp Phe Leu Ser Val Met Leu Glu Lys Gly Ser
 85           90           95
Leu Ser Ala Met Arg Phe Leu Thr Ala Val Asn Leu Glu His Pro Glu
100          105          110
Met Leu Glu Lys Ala Ser Arg Glu Leu Trp Met Arg Val Trp Ser Arg
115          120          125
Asn Glu Asp Ile Thr Glu Pro Gln Ser Ile Leu Ala Ala Ala Glu Lys
130          135          140
Ala Gly Met Ser Ala Glu Gln Ala Gln Gly Leu Leu Glu Lys Ile Ala
145          150          155          160
Thr Pro Lys Val Lys Asn Gln Leu Lys Glu Thr Thr Glu Ala Ala Cys
165          170          175
Arg Tyr Gly Ala Phe Gly Leu Pro Ile Thr Val Ala His Val Asp Gly
180          185          190
Gln Thr His Met Leu Phe Gly Ser Asp Arg Met Glu Leu Leu Ala His
195          200          205
Leu Leu Gly Glu Lys Trp Met Gly Pro Ile Pro Pro Ala Val Asn Ala
210          215          220
Arg Leu
225

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1035 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: BLADTUT04

103

(B) CLONE: 1554593

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

106

107	GGGCAGCCTC	TGCCGGGTTC	CGGGAAAAGG	AGCTCCTGCT	GCCACTGCTC	TTCCGGAGCC	60
108	TGCAGCATGG	GGCCCCTGCC	GCGCACCGTG	GAGCTCTTCT	ATGACGTGCT	GTCCCCCTAC	120
109	TCCTGGCTGG	GCTTCGAGAT	CCTGTGCCGG	TATCAGAATA	TCTGGAACAT	CAACCTGCAG	180
110	TTGCGGCCCA	GCCTCATAAC	AGGGATCATG	AAAGACAGTG	GAAACAAGCC	TCCAGGTCTG	240
111	CTTCCCCGCA	AAGGACTATA	CATGGCAAAT	GACTTAAAGC	TCCTGAGACA	CCATCTCCAG	300
112	ATTCCCATCC	ACTTCCCCAA	GGATTTCTTG	TCTGTGATGC	TTGAAAAAGG	AAGTTTGTCT	360
113	GCCATGCGTT	TCCTCACCGC	CGTGAACCTG	GAGCATCCAG	AGATGCTGGA	GAAAGCGTCC	420
114	CGGGAGCTGT	GGATGCGCGT	CTGGTCAAGG	AATGAAGACA	TCACCGAGCC	GCAGAGCATC	480
115	CTGGCGGCTG	CAGAGAAGGC	TGGTATGTCT	GCAGAACAAG	CCCAGGGACT	TCTGGAAAAG	540
116	ATCGCAACGC	CAAAGGTGAA	GAACCAGCTC	AAGGAGACCA	CTGAGGCAGC	CTGCAGATAC	600
117	GGAGCCTTTG	GGCTGCCCAT	CACCGTGGCC	CATGTGGATG	GCCAAACCCA	CATGTTATTT	660
118	GGCTCTGACC	GGATGGAGCT	GCTGGCGCAC	CTGCTGGGAG	AGAAGTGGAT	GGGCCCTATA	720
119	CCTCCAGCCG	TGAATGCCAG	ACTTTAAGAT	TGCCCCGAGG	AAGCAAATC	TTCGTATAAA	780
120	AAAAGCAGGC	CATCTGCTTA	ACCCTTGGCT	CCACCATAAG	GCACTGGGAC	TCGGATTCT	840
121	CTATCTGATA	GAGGTATTTT	CTGTGGCCCT	GGGAGCTGTC	TGTCTTTCCC	CTACCCCCAA	900
122	GGATGCCAGG	AAGACGTCCA	CCATTAGCCA	TGTGGCAACC	TTTACTTCTA	TGCCTCACAA	960
123	GTGCCTTTCA	GAGAGCCCCA	ATTCTGCTTT	CCCACAAAT	AAACCTAATG	CCATCAGGCA	1020
124	AAACAAAAAA	AAAAA					1035

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(2) INFORMATION FOR SEQ ID NO:3:

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(i) SEQUENCE CHARACTERISTICS:

129

(A) LENGTH: 226 amino acids

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(B) TYPE: amino acid

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(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

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(vii) IMMEDIATE SOURCE:

135

(A) LIBRARY: GenBank

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(B) CLONE: ?

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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140	Met	Gly	Pro	Ala	Pro	Arg	Val	Leu	Glu	Leu	Phe	Tyr	Asp	Val	Leu	Ser
141	1				5					10					15	
142	Pro	Tyr	Ser	Trp	Leu	Gly	Phe	Glu	Val	Leu	Cys	Arg	Tyr	Gln	His	Leu
143				20					25					30		
144	Trp	Asn	Ile	Lys	Leu	Lys	Leu	Arg	Pro	Ala	Leu	Leu	Ala	Gly	Ile	Met
145			35					40					45			
146	Lys	Asp	Ser	Gly	Asn	Gln	Pro	Pro	Ala	Met	Val	Pro	His	Lys	Gly	Gln
147		50					55				60					
148	Tyr	Ile	Leu	Lys	Glu	Ile	Pro	Leu	Leu	Lys	Gln	Leu	Phe	Gln	Val	Pro
149	65				70					75					80	
150	Met	Ser	Val	Pro	Lys	Asp	Phe	Phe	Gly	Glu	His	Val	Lys	Lys	Gly	Thr
151				85					90					95		
152	Val	Asn	Ala	Met	Arg	Phe	Leu	Thr	Ala	Val	Ser	Met	Glu	Gln	Pro	Glu

[illegible]

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/441,723

DATE: 02/21/2001
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/441,723

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TIME: 23:50:50

INPUT SET: S36415.raw

< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/441,723DATE: 02/21/2001
TIME: 23:50:50*INPUT SET: S36415.raw*

Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
10	(ii) TITLE OF THE INVENTION: NEW GLUTATHIONE-	(ii) TITLE OF INVENTION: NEW GLUTATHIONE-S-TR